



SEQUENCE LISTING

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<120> DIMERIZING PEPTIDES

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<151> 1999-08-11

<160> 83

<170> PatentIn Ver. 2.0

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<223> Description of Artificial Sequence: exemplary
motif characterizing C2H2 class proteins

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<221> SITE

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<223> where Xaa is any amino acid

<220>

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<223> where Xaa may be present or absent

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<223> where Xaa is any amino acid

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<223> where Xaa may be present or absent

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Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa His

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<210> 2
 <211> 4
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 subsite

<400> 2
 Asn Asn Gly Lys
 1

<210> 3
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<220>
 <223> Description of Artificial Sequence: zinc finger
 protein bind sequence

<400> 3
 ggcgtagac

9

<210> 4
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: zinc finger
 protein bind sequence

<400> 4
 ggcgacgta

9

<210> 5
 <211> 5
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<220>
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 linker

<400> 5
 Thr Gly Glu Lys Pro
 1 5

<210> 6
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<400> 6

Gly Gly Gly Gly Ser
1 5

<210> 7

<211> 8

<212> PRT

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Gly Gly Arg Arg Gly Gly Gly Ser
1 5

<210> 8

<211> 9

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Leu Arg Gln Arg Asp Gly Glu Arg Pro
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<210> 9

<211> 12

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Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

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Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
 1 5 10 15

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 finger of zinc finger protein

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<400> 11
 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa His
 20 25

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 domain F1

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 Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp
 1 5 10 15

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 site

 <400> 17
 agcatacgcc ca 12

 <210> 18
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 <212> DNA
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 site

 <400> 18
 ggaattcctg atcaagatct ggtcacgtcc ataggctagg catgtcaagg ctgtatg 57

 <210> 19
 <211> 57
 <212> DNA
 <213> Artificial Sequence

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 <400> 19
 gggatccact cggaacgcg tccttgtagt gggcgcgccc acatacagcc ttgacat 57

 <210> 20
 <211> 12
 <212> DNA
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 repeat site

 <400> 20
 tgggcgcgcc ca 12

 <210> 21
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 self-complementary oligonucleotide

 <400> 21
 atgggcgcgc ccat 14

<210> 22
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extension

<220>
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<223> "His" is numbered 89

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<222> (15)
<223> "Arg" is numbered 103

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His Pro Met Asn Asn Leu Leu Asn Tyr Val Val Pro Lys Met Arg
1 5 10 15

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<211> 34
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for affinity selection

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gcagtgggcg cgccacagt acttgaacgt aacg

34

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<400> 24
Gly Gly Gly Gln Trp Leu Gly Thr Trp Glu Trp Tyr Gly Pro Lys
1 5 10 15

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<211> 15
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<400> 25

Tyr Glu Lys Ile Ser Val Glu Gly Ile Lys Asp Val Arg Val Arg
1 5 10 15

<210> 26
<211> 15
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Asn Val Ser Ile Glu Gly Val Leu Lys Tyr Tyr Arg Gly Leu Arg
1 5 10 15

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Arg Ser Cys Gly Leu Asp Tyr Glu Gly Tyr Trp Leu Lys Leu Lys
1 5 10 15

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<211> 15
<212> PRT
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<400> 28
Ser Arg Trp Leu Glu Glu Glu Val Ser Arg Leu Leu Leu Leu Arg
1 5 10 15

<210> 29
<211> 15
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Gly Glu Ala Leu Asp Arg Phe Glu Arg Glu Met Lys Leu Met Arg
1 5 10 15

<210> 30
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      block reoptimization sequence

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Gly Gly Gly Gln Trp
  1                      5

<210> 31
<211> 5
<212> PRT
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<400> 31
His Pro Met Asn Asn
  1                      5

<210> 32
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<400> 32
Pro Pro Ser Thr Glu
  1                      5

<210> 33
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<400> 33
Gln Lys Tyr Gly Asp
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<210> 34
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<220>
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Glu Asn Tyr Glu Lys
1 5

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Leu Gly Thr Trp Glu
1 5

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Leu Leu Asn Tyr Lys
1 5

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Leu Leu Asn Tyr Val
1 5

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<400> 38
 Leu Leu Asp Tyr Ile
 1 5

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<400> 39
 Leu Leu Asn Tyr Ile
 1 5

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 Leu Leu Gln Tyr Val
 1 5

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 Leu Leu Glu Tyr Lys
 1 5

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Leu Leu Asp Tyr Val
  1                      5

<210> 43
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Leu Leu Asn Tyr Val
  1                      5

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Trp Tyr Gly Pro Lys
  1                      5

<210> 45
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His Pro Lys Met Lys
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<210> 46
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Pro Ala Lys Ile Arg

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1

5

<210> 47

<211> 5

<212> PRT

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Val Pro Lys Ser Arg

1

5

<210> 48

<211> 5

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Val Pro Arg Leu Lys

1

5

<210> 49

<211> 5

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Ala Pro Lys Leu Arg

1

5

<210> 50

<211> 5

<212> PRT

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<223> Description of Artificial Sequence: sequential
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His Ala Lys Ile Arg

1

5

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<210> 51
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Val Val Lys Met Arg
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Pro Val Lys Met Arg
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<210> 53
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Val Pro Lys Gln Arg
  1                      5

<210> 54
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Val Pro Lys Met Arg
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<210> 55
<211> 5

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Val Arg Lys Leu Arg
  1                      5

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Ser Arg Trp Leu Glu
  1                      5

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Phe Arg Trp Leu Glu
  1                      5

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Gln Pro Trp Leu Thr
  1                      5

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block reoptimization sequence

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Pro Pro Trp Leu Ile
1 5

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block reoptimization sequence

<400> 60
Pro Pro Trp Leu Lys
1 5

<210> 61
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Pro Ala Trp Leu Thr
1 5

<210> 62
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Pro Ala Trp Leu Ala
1 5

<210> 63
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block reoptimization sequence

<400> 63

Trp Ala Trp Leu Asp

1 5

<210> 64

<211> 5

<212> PRT

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Pro Thr Trp Leu Thr

1 5

<210> 65

<211> 5

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<400> 65

Glu Glu Val Ser Arg

1 5

<210> 66

<211> 5

<212> PRT

<213> Artificial Sequence

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block reoptimization sequence

<400> 66

Glu Tyr Leu Glu Ser

1 5

<210> 67

<211> 5

<212> PRT

<213> Artificial Sequence

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block reoptimization sequence

<400> 67
Asp Tyr Val Thr Gln
1 5

<210> 68
<211> 5
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<220>
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block reoptimization sequence

<400> 68
Asp Tyr Leu Ala Asp
1 5

<210> 69
<211> 5
<212> PRT
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<220>
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block reoptimization sequence

<400> 69
Glu Tyr Leu Thr Phe
1 5

<210> 70
<211> 5
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Gln Tyr Leu Glu Asp
1 5

<210> 71
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Asp Tyr Val Ser Gln

1

5

<210> 72

<211> 5

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Ser Tyr Leu Asp Lys

1

5

<210> 73

<211> 5

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<220>

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Glu Tyr Met Ser Asp

1

5

<210> 74

<211> 5

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<213> Artificial Sequence

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block reoptimization sequence

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Leu Leu Leu Leu Arg

1

5

<210> 75

<211> 5

<212> PRT

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block reoptimization sequence

<400> 75

Met Arg Leu Trp Arg

1

5

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<210> 76
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<220>
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<400> 76
Met Arg Gly Trp Lys
  1                      5

<210> 77
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<220>
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<400> 77
Met Arg Lys Trp Arg
  1                      5

<210> 78
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<220>
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<400> 78
Met Arg Lys Trp Lys
  1                      5

<210> 79
<211> 5
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<220>
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<400> 79
Met Gly Val Met Arg
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<210> 80
<211> 27

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<212> PRT
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 1 5 10 15
 Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
 20 25

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 <223> Description of Artificial Sequence: GLI1

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 Glu Thr Asp Cys Arg Trp Asp Gly Cys Ser Gln Glu Phe Asp Ser Gln
 1 5 10 15
 Glu Gln Leu Val His His Ile Asn Ser Glu His Ile
 20 25

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 <400> 82
 Glu Phe Val Cys His Trp Gly Gly Cys Ser Arg Glu Leu Arg Pro Phe
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 Lys Ala Gln Tyr Met Leu Val Val His Met Arg Arg His Thr
 20 25 30

 <210> 83
 <211> 27
 <212> PRT
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 <223> Description of Artificial Sequence: SWI5

 <400> 83
 Thr Phe Glu Cys Leu Phe Pro Gly Cys Thr Lys Thr Phe Lys Arg Arg
 1 5 10 15

Tyr Asn Ile Arg Ser His Ile Gln Thr His Leu
20 25

Bl
anal
